

FIGURE 1

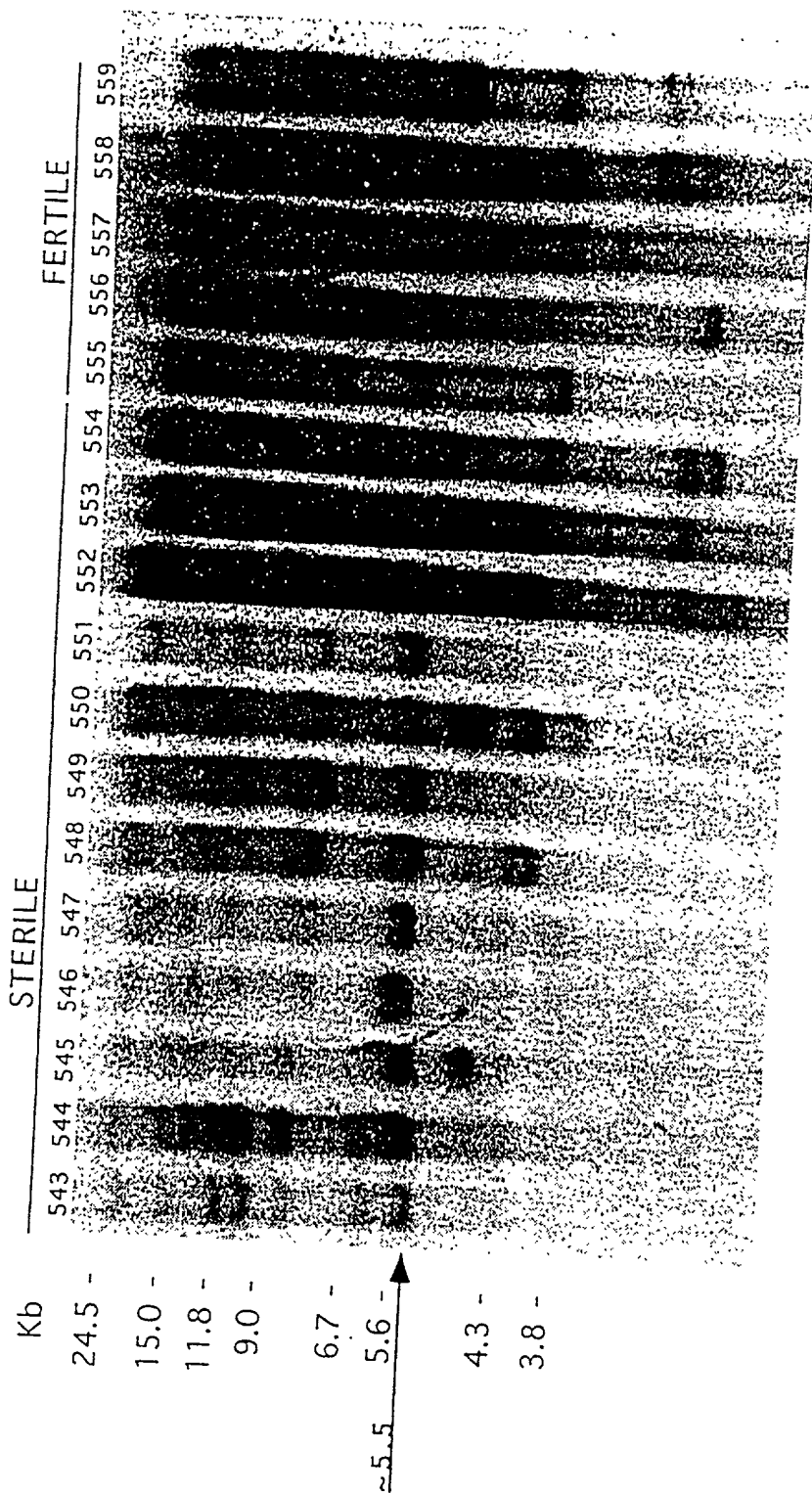


FIGURE 2

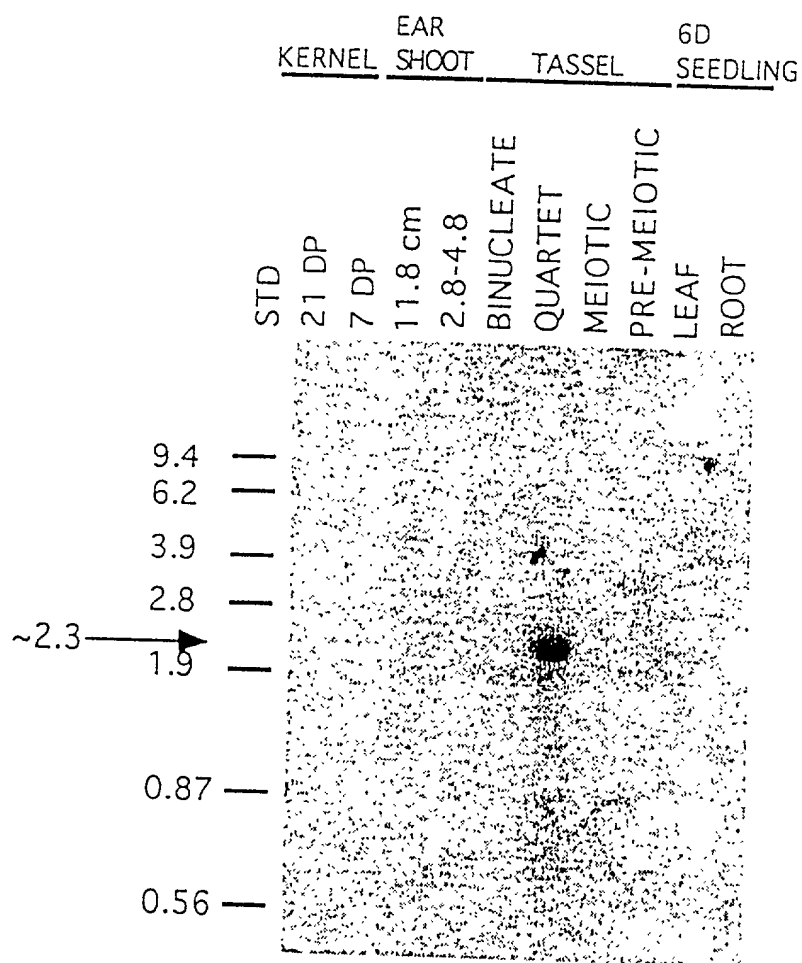


FIGURE 3

Figure 4

EcoRI
|
GAATTCGGCACGAGGGAAGCTCACCTCACGCCGGCGACGCCATCGCCATTCTTCCCACTA
1 -----+-----+-----+-----+-----+-----+ 60
CTTAAGCCGTGCTCCCTTCGAGTGGAGTGCGCCCGCTGCGGTAGCGGTAAGAAGGGTGAT

a E F G T R E A H L T P A T P S P F F P L -

GCAGGGCCTCACAAGTACATCGCGCTCCTTCTGGTTGTCCTCTCATGGATCCTGGTCCAG
61 -----+-----+-----+-----+-----+-----+ 120
CGTCCCGGAGTGTTTCATGTAGCGCGAGGAAGACCAACAGGAGAGTACCTAGGACCAGGTC

a A G P H K Y I A L L L V V L S W I L V Q -

AGGTGGAGCCTGAGGAAGCAGAAAGGCCCGAGATCATGGCCAGTCATCGGCGCAACGGTG
121 -----+-----+-----+-----+-----+-----+ 180
TCCACCTCGGACTCCTTCGTCTTTCCGGGCTCTAGTACCGGTGAGTAGCCGCGTTGCCAC

a R W S L R K Q K G P R S W P V I G A T V -

GAGCAGCTGAGGAACTACCACCGGATGCACGACTGGCTTGTCGGGTACCTGTCACGGCAC
181 -----+-----+-----+-----+-----+-----+ 240
CTCGTCGACTCCTTGATGGTGGCCTACGTGCTGACCGAACAGCCCATGGACAGTGCCGTG

a E Q L R N Y H R M H D W L V G Y L S R H -

AGGACAGTGACCGTCGACATGCCGTTCACTTCCTACACCTACATCGCTGACCCGGTGAAT
241 -----+-----+-----+-----+-----+-----+ 300
TCCTGTCACTGGCAGCTGTACGGCAAGTGAAGGATGTGGATGTAGCGACTGGGCCACTTA

a R T V T V D M P F T S Y T Y I A D P V N -

GTCGAGCATGTCTCAAGACTAACTTCACCAATTACCCCAAGGGAATCGTGACAGATCC
301 -----+-----+-----+-----+-----+-----+ 360
CAGCTCGTACAGGAGTTCTGATTGAAGTGGTTAATGGGGTTCCTTAGCACATGTCTAGG

a V E H V L K T N F T N Y P K G I V Y R S -

TACATGGACGTGCTCCTCGGTGACGGCATCTTCAACGCCGACGGCGAGCTGTGGAGGAAG
361 -----+-----+-----+-----+-----+-----+ 420
ATGTACCTGCACGAGGAGCCACTGCCGTAGAAGTTGCGGCTGCCGCTCGACACCTCCTTC

a Y M D V L L G D G I F N A D G E L W R K -

CAGAGGAAGACGGCGAGTTTCGAGTTCGCCTCCAAGAACCTGAGGGATTTTCAGCGCCATT
421 -----+-----+-----+-----+-----+-----+ 480
GTCTCCTTCTGCCGCTCAAAGCTCAAGCGGAGGTTCTTGGAAGTCCCTAAAGTCGCGGTAA

a Q R K T A S F E F A S K N L R D F S A I -

100157.494

Figure 4B

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GTGTTTCAGAGAGTACTCCCTGAAGCTGTCTGGGTATACTGAGCCAGGCATCCAAGGCAGGC
481 -----+-----+-----+-----+-----+-----+-----+ 540
CACAAGTCTCTCATGAGGGACTTCGACAGCCCATATGACTCGGTCCGTAGGTTCCGTCCG

a      V F R E Y S L K L S G I L S Q A S K A G -

AAAGTTGTGGACATGCAGGAACCTTTACATGAGGATGACGCTGGACTCCATCTGCAAGGTT
541 -----+-----+-----+-----+-----+-----+-----+ 600
TTTCAACACCTGTACGTCCTTGAAATGTACTCCTACTGCGACCTGAGGTAGACGTTCCAA

a      K V V D M Q E L Y M R M T L D S I C K V -

GGGTTCTGGGTCGAGATCGGCACGCTGTCTGCCAGATCTCCCCGAGAACAGCTTCGCGCAG
601 -----+-----+-----+-----+-----+-----+-----+ 660
CCCAAGCCCCAGCTCTAGCCGTGCGACAGCGGTCTAGAGGGGCTCTTGTCGAAGCGCGTC

a      G F G V E I G T L S P D L P E N S F A Q -

GCGTTCGATGCCGCCAACATCATCATCACGCTGCGGTTTCATCGACCCGCTGTGGCGCATC
661 -----+-----+-----+-----+-----+-----+-----+ 720
CGCAAGCTACGGCGGTTGTAGTAGTAGTGCGACGCCAAGTAGCTGGGCGACACCGCGTAG

a      A F D A A N I I I T L R F I D P L W R I -

AAGAGGTTCTTCCACGTCGGGTCTAGAGGCCCTCCTAGCGCAGAGCATCAAGCTCGTGGAC
721 -----+-----+-----+-----+-----+-----+-----+ 780
TTCTCCAAGAAGGTGCAGCCAGTCTCCGGGAGGATCGCGTCTCGTAGTTCGAGCACCTG

a      K R F F H V G S E A L L A Q S I K L V D -

GAGTTCACCTACAGCGTGATCCGCCGAGGAAGGCCGAGATCGTTCGAGGTCCGGGCCAGC
781 -----+-----+-----+-----+-----+-----+-----+ 840
CTCAAGTGGATGTCGCACTAGGCGGCCTCCTTCCGGCTCTAGCAGCTCCAGGCCCGGTGCG

a      E F T Y S V I R R R K A E I V E V R A S -

GGCAAACAGGAGAAGATGAAGCACGACATCCTGTCTACGTTTCATCGAGCTGGGCGAGGCC
841 -----+-----+-----+-----+-----+-----+-----+ 900
CCGTTTGTCTCTTCTACTTCGTGCTGTAGGACAGTGCCAAGTAGCTCGACCCGCTCCGG

a      G K Q E K M K H D I L S R F I E L G E A -

GGCGACGACGGCGGCGGCTTCGGGGACGATAAGAGCCTCCGGGACGTGGTGCTCAACTTC
901 -----+-----+-----+-----+-----+-----+-----+ 960
CCGCTGCTGCCGCCGCCGAAGCCCCTGCTATTCTCGAGGCCCTGCACCACGAGTTGAAG

a      G D D G G G F G D D K S L R D V V L N F -

GTGATCGCCGGGCGGGACACGACGGCGACGCTGTCTGTTGTTACGCACATGGCCATG
961 -----+-----+-----+-----+-----+-----+-----+ 1020
CACTAGCGGCCCGCCCTGTGCTGCCGCTGCTGCGACAGCACCAAGTGCGTGTACCGGTAC

a      V I A G R D T T A T T L S W F T H M A M -

```

1003457.400E

Variable	Mean	SD	Min	Max
Age (years)	34.2	10.5	20	55
Gender (male/female)	15/15			
Marital status (married/single)	10/5			
Occupation (student/worker)	10/5			
Education (years)	12.5	2.5	9	16
Income (TL/month)	1500	500	500	3000
Smoking status (smoker/non-smoker)	10/5			
Alcohol consumption (yes/no)	5/10			
Family size (members)	3.5	1.5	2	6
Health status (good/poor)	10/5			
Stress level (low/high)	10/5			
Life satisfaction (satisfied/dissatisfied)	10/5			
Work-life balance (good/poor)	10/5			
Overall well-being (high/low)	10/5			

	TCCCACCCCGACGTGGCCGAGAAAGCTGCCCGCGAGTGTGCGCGTTTCGAGGCGGAGCGCG	
1021	-----+-----+-----+-----+-----+-----+	1080
	AGGGTGGGCCTGCACCGGCTCTTCGACGCGGCGCTCGACACGCGCAAGCTCCGCTCGCG	
a	S H P D V A E K L R R E L C A F E A E R -	
	GCGCGCGAGGAGGGCGTCACGCTCGTGCTCTGCGGCGGCGCTGACGCCGACGACAAGGCG	
1081	-----+-----+-----+-----+-----+-----+	1140
	CGCGCGCTCCTCCCCGAGTGCGAGCACGAGACGCCGCCGCGACTGCGGCTGCTGTTCCGC	
a	A R E E G V T L V L C G G A D A D D K A -	
	TTGCCGCCCGCGTGGCGCAGTTCCGCGGCCCTCCTCACCTACGACAGCCTCGGCAAGCTG	
1141	-----+-----+-----+-----+-----+-----+	1200
	AAGCGGCGGGCGCACCGCGTCAAGCGCCCGGAGGAGTGATGCTGTGCGAGCCGTTTCGAC	
a	F A A R V A Q F A G L L T Y D S L G K L -	
	GTCTACCTCCACGCCTGCGTCACCGAGACGCTCCGCTGTACCCCGCCGTCCCTCAGGAC	
1201	-----+-----+-----+-----+-----+-----+	1260
	CAGATGGAGGTGCGGACGCAGTGCGTCTGCGAGGCGGACATGGGGCGGCAGGGAGTCCTG	
a	V Y L H A C V T E T L R L Y P A V P Q D -	
	CCCAAGGGGATCCTGGAGGACGACGTGCTGCCGGACGGGACGAAGGTGAGGGCCGGCGGG	
1261	-----+-----+-----+-----+-----+-----+	1320
	GGGTTCCCTTAGGACCTCCTGCTGCACGACGGCCTGCCCTGCTTCCACTCCCGGCCGCCC	
a	P K G I L E D D V L P D G T K V R A G G -	
	ATGGTGACGTACGTGCCCTACTCGATGGGGCGGATGGAGTACAACCTGGGGCCCCGACGCG	
1321	-----+-----+-----+-----+-----+-----+	1380
	TACCACTGCATGCACGGGATGAGCTACCCCGCTACCTCATGTTGACCCCGGGGCTGCGC	
a	M V T Y V P Y S M G R M E Y N W G P D A -	
	GCGAGCTTCCGGCCGGAGCGGTGGATCAACGAGGATGGCGCGTTCGCCAACGCGTCGCCC	
1381	-----+-----+-----+-----+-----+-----+	1440
	CGCTCGAAGGCCGGCCTCGCCACCTAGTTGCTCCTACCGCGCAAGGCGTTGCGCAGCGGC	
a	A S F R P E R W I N E D G A F R N A S P -	
	TTCAAGTTCACGGCGTTCCAGGCGGGGCCGAGGATCTGCCTGGGCAAGGACTCGGCGTAC	
1441	-----+-----+-----+-----+-----+-----+	1500
	AAGTTCAAGTGCCGCAAGGTCCGCCCCGGCTCCTAGACGGACCCGTTCTGAGCCGCATG	
a	F K F T A F Q A G P R I C L G K D S A Y -	
	CTGCAGATGAAGATGGCGCTGGCCATCCTCTTCCGCTTCTACAGCTTCCGGCTGCTGGAG	
1501	-----+-----+-----+-----+-----+-----+	1560
	GACGTCTACTTCTACCGCGACCGGTAGGAGAAGGCGAAGATGTGCAAGGCCGACGACCTC	
a	L Q M K M A L A I L F R F Y S F R L L E -	

[illegible]

2

Figure 5

1 GAATTCCAAG CGAGGCCCTT GTAGCAGAGA GTGTTGCTGA TGCAGTCGGC
51 GGAAATGAGT GCGTGCTGAG AGCAACGCTG AGGGGTTCCTA GGGATGGCAA
101 TGGCTATGGC AATCGGCTAG AGGTGGAGGA CAAGGTGGTG AGGATTGGGA
151 GGGCAACCTA TGGCAAGTTG GTGAAGAGGC ACGCAATGAG AGATCTATTC
201 AGACTTACAC TGGATGCCGC CAACAAATTC AACCTTTAGA TTTTGATACT
251 GTCACCTCCTA CTTTATTCCT TGGTTGGGCA ACTTCCAATA GGCTCATGTT
301 AATCAATGAT TAGTGATTAT TCAGCAAATA TTCTTGTTTG TTTGACATTT
351 ATAATATGTG GGGTGAGACG GATTAAATAT CATCCATGAG AGCTTTATCT
401 TCATGCTCTC TTGATTTTGG TTTCAGATCA TTCTTTCAGT GTTCACAAGA
451 ATTTTCTCAG TTTGGTCCAT GTAATTTTGG AAGTGAGGTT CCTTAAATTT
501 CATTATGCTT CCTTCTTTT CTAGACTAGC AACTGCATGA CTTTTCACCT
551 TGGGTTTACA AATTGACTCA CAAGAAAACA AATTCACCTT TGGGTTTACA
601 AATTCCTCTT CAGGATGTAC TTTTCACTTG AACTGTCATG TATAGGAACA
651 AGGAATGGCT CAGTTTTTAA GGAACAATGT ACAGATTTCA TTTCAGAACT
701 CTTTCTGGTT GGTGAGTTT CAGACTTTTT GTACCAAGCT GATGGATCAC
751 AATACTTGTT TCCAAAGTCT GATAACAGAA ACTGGCAACT CCTAATTGAT
801 AATAAAAAGA ATAAAATACA GTATCAGATA TCTCATTTTC TTGGTTGGCA
851 GATCACAAAA AGGAACACAA AGGCTAAGCC TCCTACTTGT TCGGGAGTTA
901 GGTCAGGGAC ACCATATGAA TGAAAGAAAT CTTAATTTGG GGTCACACCA
951 AGATTGTCTC TCTCGAGGTT GGGGGGTCCC TAAGGTTGGT AGTAGCAATA
1001 CCCAATATAT CACCTAACAA ACCCAATCCA TGCTACATAC ATACATAGCA
1051 TCCATCACTT GTAGACTGGA CCCTTCATCA AGAGCACCAT GGAGGAAGCT
1101 CACATCACGC CGGCGACGCC ATCGCCATTC TTCCCCTAG CAGGGCCTCA
1151 CAAGTACATC GCGCTCCTCC TGGTTGTCCT CTCATGGATC CTGGTCCAGA
1201 GGTGGAGCCT GAGGAAGCAG AAAGGCCCGA GATCATGGCC AGTCATCGGT
1251 GCAACGGTGG AGCAGCTGAG GAACTACCAC CGGATGCACG ACTGGCTTGT
1301 CGGGTACCTG TCACGGCACA GGACAGTGAC CGTCGACATG CCGTTCACTT
1351 CCTACACCTA CATCGCTGAC CCGGTGAATG TCGAGCATGT CCTCAAGACT

Figure 5B

1401 AACTTCACCA ATTACCCCAA GGTAAATGAC CTGAACTCAC TGATGTTTCAG
1451 TCTTCGGAAA TCAGAGCTGA AAGCTGAATC GAATGTGCCT GAACACCGTG
1501 TAGGGAATCG TGTACAGATC CTACATGGAC GTGCTCCTCG GTGACGGCAT
1551 CTTCAACGCC GACGGCGAGC TGTGGAGGAA GCAGAGGAAG ACGGCGAGTT
1601 TCGAGTTCGC CTCCAAGAAC CTGAGGGATT TCAGCGCCAT TGTGTTTCAGA
1651 GAGTACTCCC TGAAGCTGTC GGGTATACTG AGCCAGGCAT CCAAGGCAGG
1701 CAAAGTTGTG GACATGCAGG TGAGATCACT GCTCCCTTGC CATTGCCAAC
1751 ATGAGCATTT CAACCTGAGA CACGAGAGCT ACCTTGCCGA TTCAGGAACT
1801 TTACATGAGG ATGACGCTGG ACTCCATCTG CAAGGTTGGG TTCGGGGTCG
1851 AGATCGGCAC GCTGTCGCCG GATCTCCCCG AGAACAGCTT CGCGCAGGCG
1901 TTCGATGCCG CCAACATCAT CGTCACGCTG CGGTTTCATCG ACCCGCTGTG
1951 GCGCATCAAG AGGTTCTTCC ACGTCGGGTC AGAGGCCCTC CTAGCGCAGA
2001 GCATCAAGCT CGTGGACGAG TTCACCTACA GCGTGATCCG CCGGAGGAAG
2051 GCCGAGATCG TCGAGGCCCG GGCCAGCGGC AAACAGGAGA AGGTACGTGC
2101 ACATGACTGT TTCGATTCTT CAGTTCATCG TCTTGGCCGG GATGGACCTG
2151 ATCCTGATTG ATTATATATC CGTGTGACTT GTGAGGACAA ATTAAGATGG
2201 GCAGATGAAG CACGACATCC TGTCACGGTT CATCGAGCTA GCGGAGGCCG
2251 GCGACGACGG CGGCGGCTTC GGGGACGACA AGAGCCTCCG GGACGTGGTG
2301 CTCAACTTCG TGATCGCCGG GCGGGACACG ACGGCGACGA CGCTGTCTGT
2351 GTTCACGCAC ATGGCCATGT CCCACCCGGA CGTGGCCGAG AAGCTGCGCC
2401 GCGAGCTGTG CGCGTTCGAG GCGGAGCGCG CGCGCGAGGA GGGCGTCCGG
2451 CTCGTGCCCT GCGGCGGCGC TGACGCCGAC GACAAGGCGT TCGCCGCCCG
2501 CGTGGCGCAG TTCGCGGGCC TCCTCACCTA CGACAGCCTC GGCAAGCTGG
2551 TCTACCTCCA CGCCTGCGTC ACCGAGACGC TCCGCCTGTA CCCC GCCGTC
2601 CCTCAGGTGA GCGCGCCCGA CACGCGACCT CCGGTCCAGA GCACAGCATG
2651 CAGTGAGTGG ACCTGAATGC AATGCACATG CACTTGCGCG CGCGCAGGAC
2701 CCCAAGGGGA TCCTGGAGGA CGACGTGCTG CCGGACGGGA CGAAGGTGAG
2751 GGCCGGCGGG ATGGTGACGT ACGTGCCCTA CTCGATGGGG CGGATGGAGT

Figure 5C

2801 ACAACTGGGG CCCCGACGCG GCGAGCTTCC GGCCGGAGCG GTGGATCAAC
2851 GAGGATGGCG CGTTCCGCAA CGCGTCGCCG TTCAAGTTCA CGGCGTTCCA
2901 GGCGGGGCCG AGGATCTGCC TGGGCAAGGA CTCGGCGTAC CTGCAGATGA
2951 AGATGGCGCT GGCCATCCTC TTGCGCTTCT ACAGCTTCCG GCTGCTGGAG
3001 GGGCACCCGG TGCAGTACCG CATGATGACC ATCCTCTCCA TGGCGCACGG
3051 CCTCAAGGTC CGCGTCTCTA GGGCCGTCTG ATGTCATGGC GATTTGGGAT
3101 ATCATCCCGC TTAATCCTTA AAAATTTGCA TGCATGCATG TAAGGGAAAG
3151 CGATGGGTTT CATTGGTGGC TTGGCTTAAG CCTTAAAAAC TCCGTCGGGT
3201 CTTGCGAACC ACCACATCAC TAGTGTTTTG TACTCTACTC CTCAGTGGAA
3251 GTGTAGTGAC AGCATACAAG TTCATCATAT ATATTATCCT CTTTCTTCG
3301 CGGATGCTTC CCGGGACCTT TTGGAGACCA TTACTGACAG GCGTGTGAAA
3351 AAAAGGCTTC TTCTGCGGCG AAGTTTTGGG TTCAGAGTCT TGGCGTCTTT
3401 GCAGCAGAAA AAAGGTTTGG AAGGATCTGA ACCCTGAACC GAAAATGGCT
3451 TCGGAAATAT GCTCGCATCG GGGCGGGGCC GTCACTCGGG ATGACGACAA
3501 GCCCACAAGC AGTGAGAGCG AAGCGATCTT TGGAGTTTGG AGACACTCTC
3551 GGACCCCTCG GCGCTCCGCG AGCTCATCTT CGCCTCCTCT GTCGTGTCCG
3601 TGGCGGCACC GCGCCCGCCC GCCTCGTGTT CGACCAAATC CCGCGCCCCG
3651 ACCGTTTCGT GTACAACACC CTCATCCGCG GCGCCGCGCG CAGTGACACG
3701 CCCC GGACG CCGTATACAT CTATAAATCA TGGTATTGTA CTTTATTTTC
3751 AAACGGCCTT AACACAACCA TATTTTATG GTAAACACGT TCAAAATTGA
3801 CACAAATTTA AAACAGGCAC AAACCGTAGC TAAACATAAG AGAATGAGAG
3851 ACAACCCAAA GGTTAGAGAT GAAATAAGCT GAGTAAACGA CGAATTC

Figure 6

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1051 TCCATCACTTGTAGACTGGACCCTTCATCAAGAGCACCATGGAGGAAGCT 1100
      | | | | |
1   .....GAATTCGGCACGAGGGAAGCT 21

1101 CACATCACGCCGGCGACGCCATCGCCATTCTTCCCACTAGCAGGGCCTCA 1150
      | | | | |
22  CACCTCACGCCGGCGACGCCATCGCCATTCTTCCCACTAGCAGGGCCTCA 71

1151 CAAGTACATCGCGCTCCTCCTGGTTGTCCTCTCATGGATCCTGGTCCAGA 1200
      | | | | |
72  CAAGTACATCGCGCTCCTCCTGGTTGTCCTCTCATGGATCCTGGTCCAGA 121

1201 GGTGGAGCCTGAGGAAGCAGAAAGGCCCGAGATCATGGCCAGTCATCGGT 1250
      | | | | |
122 GGTGGAGCCTGAGGAAGCAGAAAGGCCCGAGATCATGGCCAGTCATCGGC 171

1251 GCAACGGTGGAGCAGCTGAGGAACTACCACCGGATGCACGACTGGCTTGT 1300
      | | | | |
172 GCAACGGTGGAGCAGCTGAGGAACTACCACCGGATGCACGACTGGCTTGT 221

1301 CGGGTACCTGTACGGCACAGGACAGTGACCGTCGACATGCCGTTCACTT 1350
      | | | | |
222 CGGGTACCTGTACGGCACAGGACAGTGACCGTCGACATGCCGTTCACTT 271

1351 CCTACACCTACATCGCTGACCCGGTGAATGTCGAGCATGTCCTCAAGACT 1400
      | | | | |
272 CCTACACCTACATCGCTGACCCGGTGAATGTCGAGCATGTCCTCAAGACT 321

1401 AACTTCACCAATTACCCCAAGGTAAATGACCTGAACTCACTGATGTTTCA 1450
      | | | | |
322 AACTTCACCAATTACCCCA..... 340

      .
      .

1501 TAGGGAATCGTGACAGATCCTACATGGACGTGCTCCTCGGTGACGGCAT 1550
      | | | | |
341 .AGGGAATCGTGACAGATCCTACATGGACGTGCTCCTCGGTGACGGCAT 389

1551 CTTCAACGCCGACGGCGAGCTGTGGAGGAAGCAGAGGAAGACGGCGAGTT 1600
      | | | | |
390 CTTCAACGCCGACGGCGAGCTGTGGAGGAAGCAGAGGAAGACGGCGAGTT 439

1601 TCGAGTTCGCCTCCAAGAACCTGAGGGATTTAGCGCCATTGTGTTTCA 1650
      | | | | |
440 TCGAGTTCGCCTCCAAGAACCTGAGGGATTTAGCGCCATTGTGTTTCA 489

1651 GAGTACTCCCTGAAGCTGTGGGTATACTGAGCCAGGCATCCAAGGCAGG 1700
      | | | | |
490 GAGTACTCCCTGAAGCTGTGGGTATACTGAGCCAGGCATCCAAGGCAGG 539

1701 CAAAGTTGTGGACATGCAGGTGAGATCACTGCTCCCTTGCCATTGCCAAC 1750
      | | | | |
540 CAAAGTTGTGGACATG..... 555

```

Figure 6B

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1751 ATGAGCATTTC AACCTGAGACACGAGAGCTACCTTGCCGATT CAGGAACT 1800
      |||||
556 ..... CAGGAACT 563

1801 TTACATGAGGATGACGCTGGACTCCATCTGCAAGGTTGGGTTCTGGGGTCG 1850
      |||||
564 TTACATGAGGATGACGCTGGACTCCATCTGCAAGGTTGGGTTCTGGGGTCG 613

1851 AGATCGGCACGCTGTCTGCCGGATCTCCCCGAGAACAGCTTCGCGCAGGCG 1900
      |||||
614 AGATCGGCACGCTGTCTGCCAGATCTCCCCGAGAACAGCTTCGCGCAGGCG 663

1901 TTCGATGCCGCCAACATCATCTGTCACGCTGCGGTTTCATCGACCCGCTGTG 1950
      |||||
664 TTCGATGCCGCCAACATCATCTGTCACGCTGCGGTTTCATCGACCCGCTGTG 713

1951 GCGCATCAAGAGGTTCTTCCACGTCGGGTCTAGAGGCCCTCCTAGCGCAGA 2000
      |||||
714 GCGCATCAAGAGGTTCTTCCACGTCGGGTCTAGAGGCCCTCCTAGCGCAGA 763

2001 GCATCAAGCTCGTGGACGAGTTACCTACAGCGTGATCCGCCGAGGAAG 2050
      |||||
764 GCATCAAGCTCGTGGACGAGTTACCTACAGCGTGATCCGCCGAGGAAG 813

2051 GCCGAGATCGTCTGAGGCCCCGGGCCAGCGGCAAACAGGAGAAGGTACGTGC 2100
      |||||
814 GCCGAGATCGTCTGAGGTCCGGGCCAGCGGCAAACAGGAGA..... 853

      .
      .

2201 GCAGATGAAGCACGACATCTGTACGCGTTTCATCGAGCTAGGCGAGGCCG 2250
      |||||
854 ..AGATGAAGCACGACATCTGTACGCGTTTCATCGAGCTAGGCGAGGCCG 901

2251 GCGACGACGGCGGGCGGCTTCGGGGACGACAAGAGCCTCCGGGACGTGGTG 2300
      |||||
902 GCGACGACGGCGGGCGGCTTCGGGGACGATAAGAGCCTCCGGGACGTGGTG 951

2301 CTCAACTTCGTGATCGCCGGGCGGGACACGACGGCGACGACGCTGTCTGTG 2350
      |||||
952 CTCAACTTCGTGATCGCCGGGCGGGACACGACGGCGACGACGCTGTCTGTG 1001

2351 GTTCACGCACATGGCCATGTCCCACCCGACGTGGCCGAGAAGCTGCGCC 2400
      |||||
1002 GTTCACGCACATGGCCATGTCCCACCCGACGTGGCCGAGAAGCTGCGCC 1051

2401 GCGAGCTGTGCGCGTTTCGAGGCGGAGCGCGCGCGAGGAGGGCGTCGCG 2450
      |||||
1052 GCGAGCTGTGCGCGTTTCGAGGCGGAGCGCGCGCGAGGAGGGCGTCACG 1101

2451 CTCGTGCCCTGCGGCGGGCGCTGACGCCGACGACAAGGCGTTTCGCCGCCCG 2500
      |||||
1102 CTCGTGCTCTGCGGCGGGCGCTGACGCCGACGACAAGGCGTTTCGCCGCCCG 1151

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Figure 6C

2501 CGTGGCGCAGTTCGCGGGCCTCCTCACCTACGACAGCCTCGGCAAGCTGG 2550
 |||
 1152 CGTGGCGCAGTTCGCGGGCCTCCTCACCTACGACAGCCTCGGCAAGCTGG 1201
 2551 TCTACCTCCACGCCTGCGTCACCGAGACGCTCCGCCTGTACCCCGCCGTC 2600
 |||
 1202 TCTACCTCCACGCCTGCGTCACCGAGACGCTCCGCCTGTACCCCGCCGTC 1251
 2601 CCTCAGGTGAGCGCGCCCCACACGCGACCTCCGGTCCAGAGCACAGCATG 2650
 |||
 1252 CCT..... 1254
 2651 CAGTGAGTGGACCTGAATGCAATGCACATGCACTTGCGCGCGCGCAGGAC 2700
 |||
 1255CAGGAC 1260
 2701 CCCAAGGGGATCCTGGAGGACGACGTGCTGCCGGACGGGACGAAGGTGAG 2750
 |||
 1261 CCCAAGGGGATCCTGGAGGACGACGTGCTGCCGGACGGGACGAAGGTGAG 1310
 2751 GGCCGGCGGGATGGTGACGTACGTGCCCTACTCGATGGGGCGGATGGAGT 2800
 |||
 1311 GGCCGGCGGGATGGTGACGTACGTGCCCTACTCGATGGGGCGGATGGAGT 1360
 2801 ACAACTGGGGCCCCGACGCGGCGAGCTTCGGCCGGAGCGGTGGATCAAC 2850
 |||
 1361 ACAACTGGGGCCCCGACGCGGCGAGCTTCGGCCGGAGCGGTGGATCAAC 1410
 2851 GAGGATGGCGCGTTCGCAACGCGTCGCCGTTCAAGTTCACGGCGTTCCA 2900
 |||
 1411 GAGGATGGCGCGTTCGCAACGCGTCGCCGTTCAAGTTCACGGCGTTCCA 1460
 2901 GGCGGGGCGGAGGATCTGCCTGGGCAAGGACTCGGCGTACCTGCAGATGA 2950
 |||
 1461 GGCGGGGCGGAGGATCTGCCTGGGCAAGGACTCGGCGTACCTGCAGATGA 1510
 2951 AGATGGCGCTGGCCATCCTCTTGCCTTCTACAGCTTCCGGCTGCTGGAG 3000
 |||
 1511 AGATGGCGCTGGCCATCCTCTTGCCTTCTACAGCTTCCGGCTGCTGGAG 1560
 3001 GGGCACCCGGTGCAGTACCGCATGATGACCATCCTCTCCATGGCGCACGG 3050
 |||
 1561 GGGCACCCGGTGCAGTACCGCATGATGACCATCCTCTCCATGGCGCACGG 1610
 3051 CCTCAAGGTCCGCGTCTCTAGGGCCGTCTGATGTCATGGCGATTTG.... 3096
 |||
 1611 CCTCAAGGTCCGCGTCTCTAGGGCCGTCTGATGTCATGGCGATTTGGATA 1660
 3097 .GGATATCATCCCGCTTAATCC.....TTAAAAATT 3126
 |||
 1661 TGGATATCGTCCCGCTTAATCCACGACAAATAACGCTCGTGTACAAATT 1710
 3127 TGCATGCATGCATGTAAGGGAAAGCGATGGGTTTCATTGGTGGCTTGGCT 3176
 |||
 1711 TGCATGCATGCATGTAAGGGAAAGCGATGGGTTTCATTGGTGGCTTGGCT 1760

Figure 6D

3177 TAAGCCTTAAAACTCCGTCGGGTCTTGCGAACCACCACATCACTAGTGT 3226
|||||
1761 TAAGCCTTAAAACTCCGTCGGGTCTTGCGAACCACCACATCACTAGTGT 1810
3227 TTTGTACTCTACTCCTCAGTGGAGTGTAGTGACAGCATACAAGTTCATC 3276
|||||
1811 TTTGTACTCTACTCCTCAGTGGAGTGTAGTGACAGCATACAAGTTCATC 1860
3277 ATATATATTATCCTCTTTCTTCGCCGGATGCTTCCCGGGACCTTTTGGAG 3326
|||||
1861 ATATATATTATCCTCTTTCTTAAAAAAAAAAAAAAAAAACTCGAG.... 1906

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1003457.12401

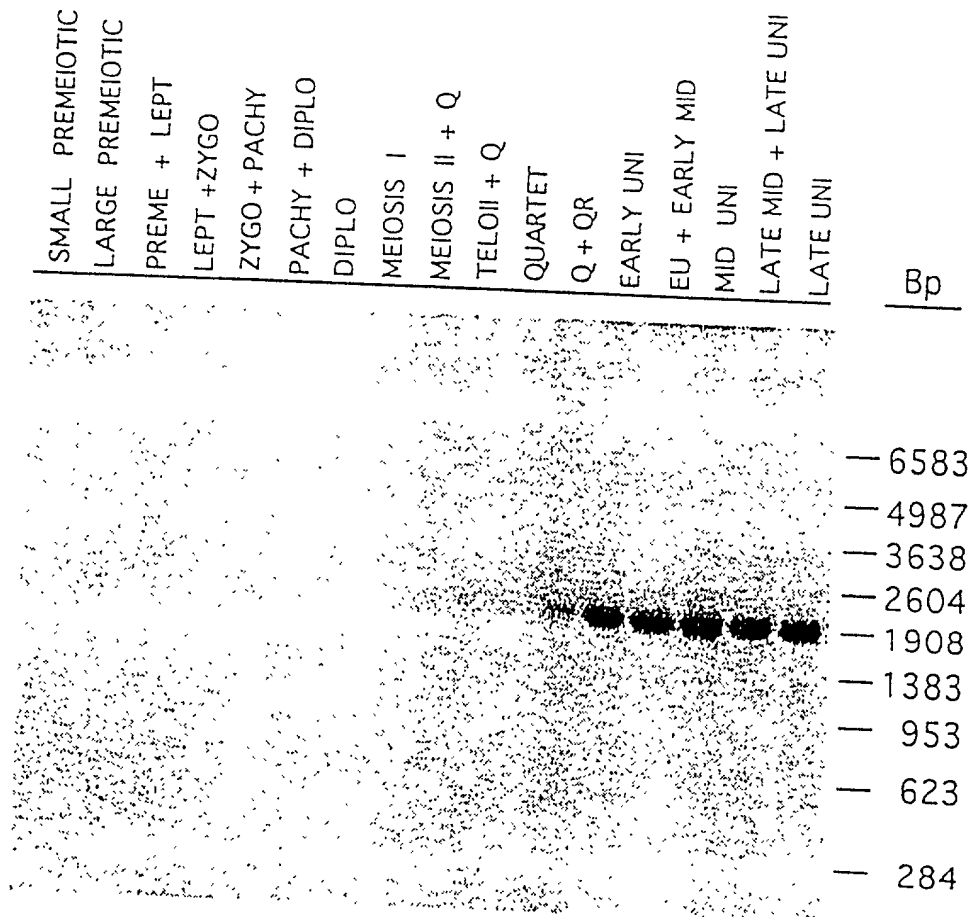


Figure 7

Figure 8

1 GAATTCCAAG CGAGGCCCTT GTAGCAGAGA GTGTTGCTGA TGCAGTCGGC
51 GGAAATGAGT GCGTGCTGAG AGCAACGCTG AGGGGTTCCA GGGATGGCAA
101 TGGCTATGGC AATCGGCTAG AGGTGGAGGA CAAGGTGGTG AGGATTGGGA
151 GGGCAACCTA TGGCAAGTTG GTGAAGAGGC ACGCAATGAG AGATCTATTC
201 AGACTTACAC TGGATGCCGC CAACAAATTC AACCTTTAGA TTTTGATACT
251 GTCACTCCTA CTTTATTCCT TGGTTGGGCA ACTTCCAATA GGCTCATGTT
301 AATCAATGAT TAGTGATTAT TCAGCAAATA TTCTTGTTTG TTTGACATTT
351 ATAATATGTG GGGTGAGACG GATTAAATAT CATCCATGAG AGCTTTATCT
401 TCATGCTCTC TTGATTTTGG TTTCAGATCA TTCTTTCAGT GTTCACAAGA
451 ATTTTCTCAG TTTGGTCCAT GTAATTTTTG AAGTGAGGTT CCTTAAATTT
501 CATTATGCTT CCTTTCTTTT CTAGACTAGC AACTGCATGA CTTTTCACCT
551 TGGGTTTACA AATTGACTCA CAAGAAAACA AATTCACCTT TGGGTTTACA
601 AATTCCTCTT CAGGATGTAC TTTTCACTTG AACTGTCATG TATAGGAACA
651 AGGAATGGCT CAGTTTTTAA GGAACAATGT ACAGATTTCA TTTCAGAACT
701 CTTTCTGGTT GGTTGAGTTT CAGACTTTTT GTACCAAGCT GATGGATCAC
751 AATACTTGTT TCCAAAGTCT GATAACAGAA ACTGGCAACT CCTAATTGAT
801 AATAAAAAGA ATAAAATACA GTATCAGATA TCTCATTTTC TTGGTTGGCA
851 GATCACAAAA AGGAACACAA AGGCTAAGCC TCCTACTTGT TCGGGAGTTA
901 GGTCAGGGAC ACCATATGAA TGAAAGAAAT CTTAATTGG GTTCACACCA
951 AGATTGTCTC TCTCGAGGTT GGGGGGTCCC TAAGGTTGGT AGTAGCAATA
1001 CCCAATATAT CACCTAACAA ACCCAATCCA TGCTACATAC ATACATAGCA
1051 TCCATCACTT GTAGACTGGA CCCTTCATCA AGAGCACCAT GG

SBMu200 Promoter Analysis: 5' Deletions

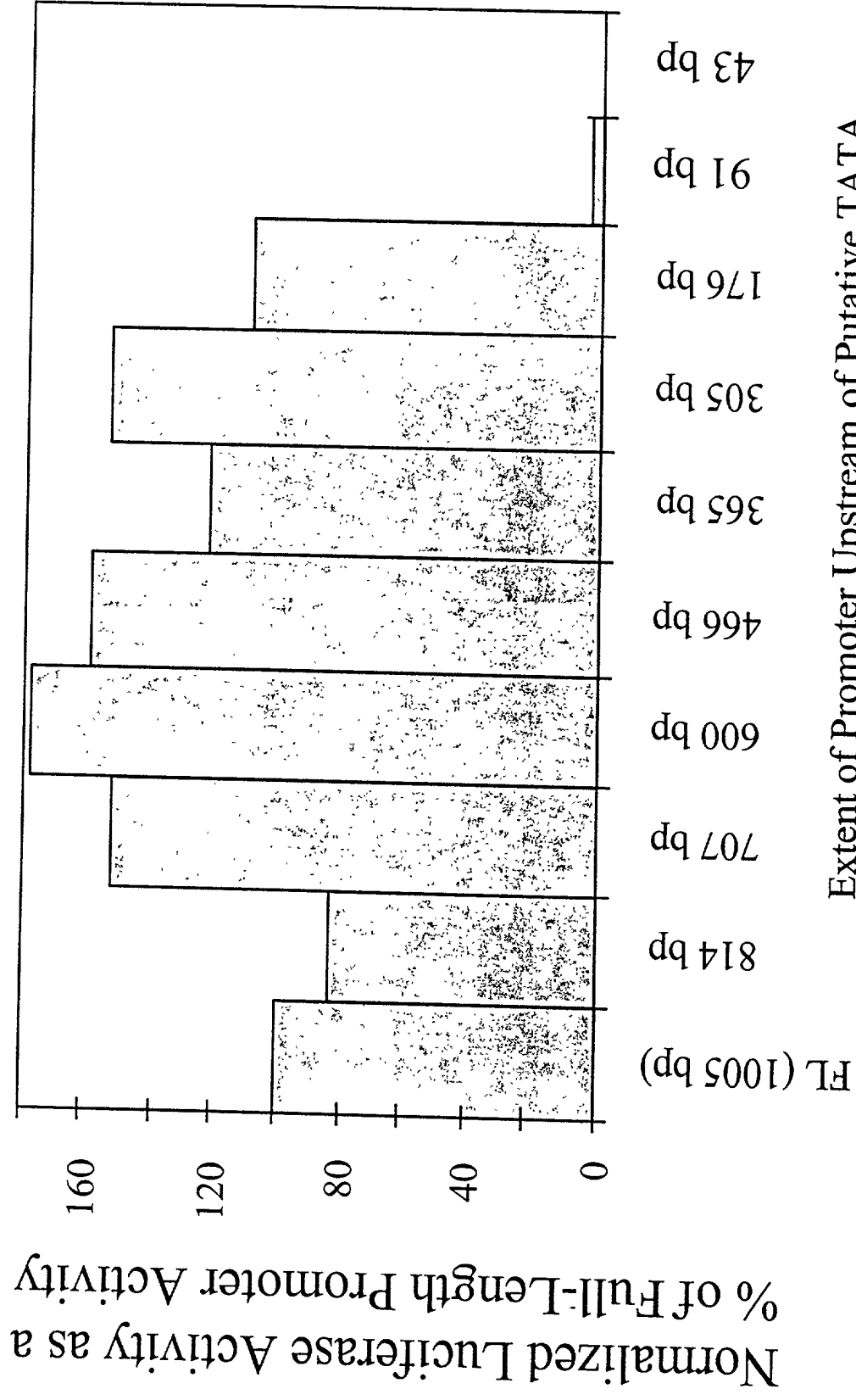


Figure 9

SBMu200 “Minimal” Promoter

-180	CCC	<u>ATCTCA</u>	LS01	LS02	LS03	LS04	LS05
		TTTTCTTGGT					
		TGGCAGATCA					
		CAAAAAGGAA					
		CACAAAGGCT					
-130	AAGCCTCCTA	CTTGTTCTGGG	LS06	LS07	LS08	LS09	LS10
		AGTTAGGTCA					
		GGGACACCAT					
		ATGAATGAAA					
-80	GAAATCTTAA	TTTGGGGGTCA	LS11	LS12	LS13	LS14	LS15
		CACCAAGATT					
		GTCCTCTCG					
		TCG					
-30	GTCCCTAAGG	TTGGTAGTAG	LS16	LS17	LS18		
		CAATACCCAA					
		TATATCACCT					
		AACAAACCCA					
20	ATCCATGCTA	CATACATACA					
		TAGCATCCAT					
		CACCTGTAGA					
		CTGGACCCTT					
70	CATCAAGAGC	ACCATGG					

Coordinates are relative to the putative TATA box (underlined). P motifs are in *italic*.
 [] = Del -176/-92 [] = Del -89/-44 [] = Del -39/-8
 Linker scanning mutations that reduce activity to ~5% or less are in **bold**. Mutations with a significant but less pronounced effect are in **bold italic**.

Figure 10

Linker Scanning Analysis of SBMu200 Promoter

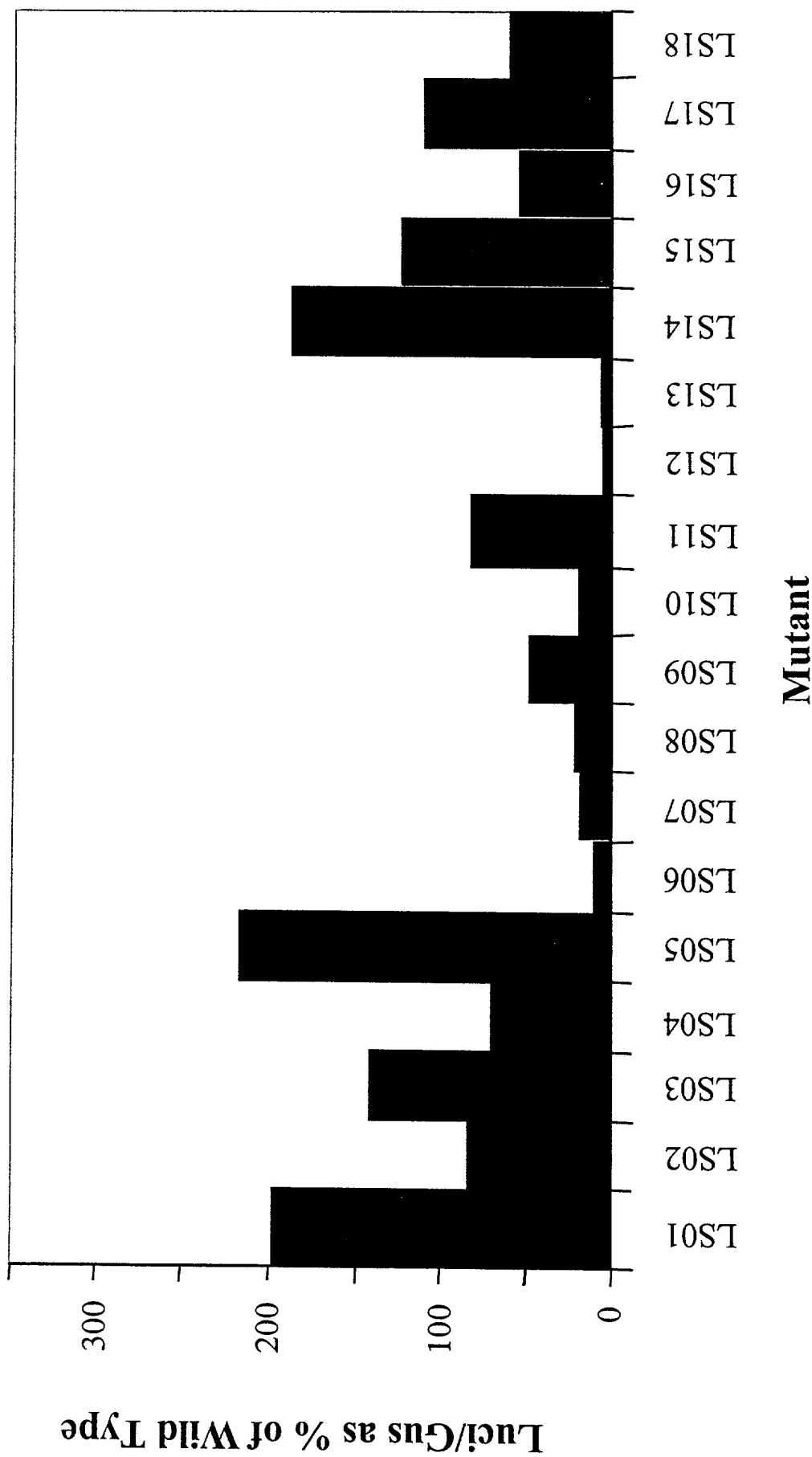


Figure 11

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100																																																		
Population	1000000	1050000	1100000	1150000	1200000	1250000	1300000	1350000	1400000	1450000	1500000	1550000	1600000	1650000	1700000	1750000	1800000	1850000	1900000	1950000	2000000	2050000	2100000	2150000	2200000	2250000	2300000	2350000	2400000	2450000	2500000	2550000	2600000	2650000	2700000	2750000	2800000	2850000	2900000	2950000	3000000	3050000	3100000	3150000	3200000	3250000	3300000	3350000	3400000	3450000	3500000	3550000	3600000	3650000	3700000	3750000	3800000	3850000	3900000	3950000	4000000	4050000	4100000	4150000	4200000	4250000	4300000	4350000	4400000	4450000	4500000	4550000	4600000	4650000	4700000	4750000	4800000	4850000	4900000	4950000	5000000	5050000	5100000	5150000	5200000	5250000	5300000	5350000	5400000	5450000	5500000	5550000	5600000	5650000	5700000	5750000	5800000	5850000	5900000	5950000	6000000	6050000	6100000	6150000	6200000	6250000	6300000	6350000	6400000	6450000	6500000	6550000	6600000	6650000	6700000	6750000	6800000	6850000	6900000	6950000	7000000	7050000	7100000	7150000	7200000	7250000	7300000	7350000	7400000	7450000	7500000	7550000	7600000	7650000	7700000	7750000	7800000	7850000	7900000	7950000	8000000	8050000	8100000	8150000	8200000	8250000	8300000	8350000	8400000	8450000	8500000	8550000	8600000	8650000	8700000	8750000	8800000	8850000	8900000	8950000	9000000	9050000	9100000	9150000	9200000	9250000	9300000	9350000	9400000	9450000	9500000	9550000	9600000	9650000	9700000	9750000	9800000	9850000	9900000	9950000	10000000

Percent Similarity: 92.510 Percent Identity: 90.891
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87 MPFTSYTYIADPVNVEHVLKTNFTNYPKGIVYRSYMDVLLGDGIFNADGE 136
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55 LWRKQRKTASF EFASKNLRDFSANVFREYSLKLSGILSQASKAGKVVDQM 104
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10157

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155 LWRIQKFF 162
    |||.:.||
237 LWRIKRFF 244

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